GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 1, 2002, 06:24:15 ; Search time 32.44 Seconds
(without alignments)
1222.360 Million cell updates/sec

Title: US-09-522-752-2
Perfect score: 1854
Sequence: 1 MADDYGSESTSSMEDYVNFN.....EGSLKLSSMLLETTSGALSL 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*
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19: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1998.DAT:*
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21: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1854	100.0	357	21	AAB19605	Human CC chemokine
2	1854	100.0	357	21	AAY90615	Human G protein-co
3	1854	100.0	357	22	AAG80117	Human CCR9b protei
4	1854	100.0	369	22	AAG80116	Human CCR9a protei
5	1848	99.7	357	21	AAY90649	Human mutant G pro
6	1848	99.7	369	22	ABB56344	Non-endogenous hum
7	780.5	42.1	358	15	AAR53745	Partial sequence o
8	780.5	42.1	358	21	AAB21689	Human 7TM receptor
9	780.5	42.1	378	19	AAW48724	Human V31 seven tr
10	780.5	42.1	378	21	AAB21688	Human 7TM receptor
11	780.5	42.1	378	21	AAY90629	Human G protein-co
12	780.5	42.1	378	22	AAG80114	Human CCR7 protein
13	780.5	42.1	378	22	AAB50859	Human CCR7. Homo
14	780.5	42.1	410	15	AAR53743	Putative seven tra
15	780.5	42.1	410	19	AAW48723	Polypeptide sequen
16	780.5	42.1	410	21	AAB21687	Genomic clone of 7
17	780.5	42.1	569	22	ABG12373	Novel human diagno
18	777.5	41.9	378	15	AAR53744	Putative seven tra
19	776.5	41.9	378	21	AAY90663	Human mutant G pro
20	758.5	40.9	378	15	AAR54079	Epstein Barr virus
21	758.5	40.9	378	19	AAW56164	G-protein coupled
22	758.5	40.9	378	19	AAW53622	Epstein Barr virus
23	757.5	40.9	378	21	AAB21699	7TM receptor prote
24	742	40.0	359	15	AAR53747	Seven transmembran
25	742	40.0	359	19	AAW48728	Murine V31 seven t
26	742	40.0	359	21	AAB21691	Murine 7TM recepto
27	721	38.9	361	20	AAW97348	An Epstein-barr vi
28	671.5	36.2	351	20	AAY23825	A7 times membrane
29	652	35.2	350	22	AAG67238	Amino acid sequenc
30	640	34.5	350	20	AAY57291	Mouse BGCKr protei
31	638.5	34.4	369	22	AAG80113	Human CCR6b protei
32	638.5	34.4	374	22	AAG80112	Human CCR6a protei
33	637	34.4	349	20	AAW93170	Human HFIAO41 prot
34	637	34.4	350	20	AAY57290	Human BGCKr protei
35	637	34.4	350	20	AAY30125	A human seven-pass
36	637	34.4	350	20	AAY17435	Human signal pepti
37	637	34.4	350	20	AAW93169	Human HFIAO41 prot
38	637	34.4	350	21	AAY94325	Human seven transm
39	637	34.4	350	22	AAG80119	Human CCR11 protei
40	637	34.4	350	22	AAU08994	Human G protein-co
41	637	34.4	350	22	AAG67237	Amino acid sequenc
42	637	34.4	382	22	AAB62389	Human chemokine re
43	635	34.3	333	20	AAY57289	Human BGCKr partia
44	632	34.1	350	21	AAY71301	Human orphan G pro
45	632	34.1	350	21	AAB02835	Human G protein co

ALIGNMENTS

RESULT 1
AAB19605
ID AAB19605 standard; Protein; 357 AA.
XX
AC AAB19605;
XX
DT 22-JAN-2001 (first entry)
XX
DE Human CC chemokine receptor GPR-9-6.
XX
KW GPR-9-6; human; chemokine receptor; TECK; cancer; leukaemia;
KW lymphoma; carcinoma; inflammation; Crohn's disease; colitis;
KW therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO200053635-A1.
XX
PD 14-SEP-2000.
XX
PF 10-MAR-2000; 2000WO-US06240.
XX
PR 11-MAR-1999; 99US-0266464.
XX
PA (LEUK-) LEUKOSITE INC.
XX
PI Andrew DP, Zabel BA, Ponath PD;
XX
DR WPI; 2000-572263/53.
XX
PT Antibody or its antigen-binding fragment which binds to the mammalian
PT CC chemokine receptor GPR-9-6, useful for treating inflammatory
PT diseases, cancer or inhibiting GPR-9-6-mediated homing of leukocytes to
PT mucosal tissue -

XX
PS Disclosure; Fig 14A-B; 114pp; English.
XX
CC The present sequence is that of human GPR-9-6, a CC chemokine
CC receptor that is expressed on the majority of thymocytes and also
CC on a subset of memory CD4 lymphocytes that traffic to mucosal
CC sites, suggesting a dual role in T cell development and mucosal
CC immune response. The invention relates to an antibody that binds
CC to GPR-9-6 and blocks the binding of a ligand, such as TECK (see
CC AAB19607), to the receptor. Also provided is a method of identifying
CC agents which can bind to GPR-9-6 and inhibit the binding of a
CC ligand and/or modulate a function of GPR-9-6. The antibodies can
CC be used to detect or measure expression of GPR-9-6 receptor. They
CC are useful for treating an inflammatory disease, cancer and
CC inhibiting GPR-9-6-mediated homing of leukocytes to mucosal tissue.
CC The cancer treated is acute or chronic leukaemia (e.g., acute T-cell
CC lymphoblastic leukaemia, acute B-cell lymphoblastic leukaemia,
CC chronic T-cell lymphoblastic leukaemia, chronic B-cell lymphoblastic
CC leukaemia), lymphoma (e.g., Hodgkin's disease, T cell lymphoma) or
CC carcinoma (e.g. breast, melanoma, myeloma, or adenoma). The
CC inflammatory diseases treated are Crohn's disease, colitis
CC (claimed), inflammatory bowel disease, mastitis, vaginitis,
CC cholangitis or pericholangitis, chronic bronchitis, asthma, graft
CC versus host disease, hypersensitivity pneumonitis, collagen
CC diseases, sarcoidosis, and other idiopathic conditions. Other
CC diseases that can be treated by the antibodies are autoimmune
CC diseases (e.g. rheumatoid arthritis, multiple sclerosis), infectious
CC diseases (e.g. bacterial and viral infections), atherosclerosis,
CC restenosis, AIDS, pancreatitis, insulin-dependent diabetes mellitus,
CC and diseases in which angiogenesis or neovascularization play a role.
XX
SQ Sequence 357 AA;

Query Match 100.0%; Score 1854; DB 21; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 60

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
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Db     121 cvllimcisvdryiaiaqamrahtwrekrllyskmvcftiwvlaaalcipeilysqikee 180

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
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Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
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RESULT 2
AAY90615
ID AAY90615 standard; Protein; 357 AA.
XX
AC AAY90615;
XX
DT 21-AUG-2000 (first entry)
XX
DE Human G protein-coupled receptor GPR9-6.
XX
KW G protein-coupled receptor; GPCR; constitutively active;
KW intracellular loop 3; transmembrane domain 6; drug screening;
KW agonist; antagonist.
XX
OS Homo sapiens.
XX
PN WO200022129-A1.
XX
PD 20-APR-2000.
XX
PF 12-OCT-1999; 99WO-US23938.
XX
PR 13-OCT-1998; 98US-0170496.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Behan DP, Chalmers DT, Liaw CW;
XX
DR WPI; 2000-329165/28.
DR N-PSDB; AAA30596.
XX
PT Non-endogenous constitutively activated human G protein-coupled
PT receptors, useful for identifying agonists for use as pharmaceutical
PT agents -
XX
PS Example 1; Page 119-120; 341pp; English.
XX
CC The invention relates to constitutively active, non-endogenous versions
CC of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC and AAA30775-A30779). The mutant proteins of the invention contain a
CC mutation in a portion of the protein comprising intracellular loop 3
CC (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC is substituted for an endogenous residue in IC3 at a position 16 amino
CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents a human wild-type GPCR referred
CC to in an exemplification of the invention.
XX
SQ Sequence 357 AA;

Query Match 100.0%; Score 1854; DB 21; Length 357;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 357; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 60

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Db      61 ywyctrvktmtdmfllnlaiadllflvtlpfwaiaaadqwkfqtfmckvvnsmykmnfys 120

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
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Db     121 cvllimcisvdryiaiaqamrahtwrekrllyskmvcftiwvlaaalcipeilysqikee 180

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
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Db    301 npvlyvfvgerfrrdlvktlknlgcisqaqwvsftrregslklssmllettsgalsl 357


RESULT   3
AAG80117
ID   AAG80117 standard; Protein; 357 AA.
XX
AC   AAG80117;
XX
DT   17-JAN-2002  (first entry)
XX
DE   Human CCR9b protein.
XX
KW   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW   inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW   chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW   antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW   antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200172830-A2.
XX
PD   04-OCT-2001.
XX
PF   02-APR-2001; 2001WO-EP03708.
XX
PR   31-MAR-2000; 2000DE-1016013.
XX
PA   (IPFP-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
XX
PI   Forssmann W,  Adermann K,  Heitland A,  Spodsberg N;
XX
DR   WPI; 2001-626256/72.
XX
PT   Diagnostic agent containing two or more receptor-specific ligands,
PT   useful for detecting tumors, inflammation etc., also therapeutic use of
PT   ligand inhibitors  -
XX
PS   Disclosure; Page 11; 26pp; German.
XX
CC   This invention describes a novel diagnostic agent (A) comprising at least
CC   two different ligands (I) for receptors (II) that are implicated in
CC   disease. (A) are used for the diagnosis of tumors (especially colorectal
CC   or prostatic), organ rejection, inflammation and autoimmune diseases.
CC   Also inhibitors of (I) are used therapeutically against tumors (and their
CC   metastases), inflammation (particularly bronchial asthma or chronic bowel
CC   inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC   where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC   endocrine, motor or urogenital systems or skin are affected, and bone
CC   marrow diseases. The products of the invention are chemokine derivatives
CC   which have cytostatic, antiinflammatory, antiasthmatic,
CC   immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC   Chemokines act on specific tumor and inflammatory cells through a
CC   constellation of chemokine receptors (CR), which control migration and
CC   proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC   fragments used to illustrate the method of the invention.
XX
SQ   Sequence   357 AA;

  Query Match             100.0%;  Score 1854;  DB 22;  Length 357;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-191;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 60

Qy     61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Db     61 ywyctrvktmtdmfllnlaiadllflvtlpfwaiaaadqwkfqtfmckvvnsmykmnfys 120

Qy    121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
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Db    121 cvllimcisvdryiaiaqamrahtwrekrllyskmvcftiwvlaaalcipeilysqikee 180

Qy    181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
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Db    181 sgiaictmvypsdestklksavltlkvilgfflpfvvmaccytiiihtliqakkssknka 240

Qy    241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
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Db    241 lkvtitvltvfvlsqfpyncillvqtidayamfisncavstnidicfqvtqtiaffhscl 300

Qy    301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
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Db    301 npvlyvfvgerfrrdlvktlknlgcisqaqwvsftrregslklssmllettsgalsl 357


RESULT   4
AAG80116
ID   AAG80116 standard; Protein; 369 AA.
XX
AC   AAG80116;
XX
DT   17-JAN-2002  (first entry)
XX
DE   Human CCR9a protein.
XX
KW   Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW   inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW   chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW   antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW   antirheumatic; antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200172830-A2.
XX
PD   04-OCT-2001.
XX
PF   02-APR-2001; 2001WO-EP03708.
XX
PR   31-MAR-2000; 2000DE-1016013.
XX
PA   (IPFP-) IPF PHARM GMBH.
PA   (FORS/) FORSSMANN U.
XX
PI   Forssmann W,  Adermann K,  Heitland A,  Spodsberg N;
XX
DR   WPI; 2001-626256/72.
XX
PT   Diagnostic agent containing two or more receptor-specific ligands,
PT   useful for detecting tumors, inflammation etc., also therapeutic use of
PT   ligand inhibitors  -
XX
PS   Disclosure; Page 11; 26pp; German.
XX
CC   This invention describes a novel diagnostic agent (A) comprising at least
CC   two different ligands (I) for receptors (II) that are implicated in
CC   disease. (A) are used for the diagnosis of tumors (especially colorectal
CC   or prostatic), organ rejection, inflammation and autoimmune diseases.
CC   Also inhibitors of (I) are used therapeutically against tumors (and their
CC   metastases), inflammation (particularly bronchial asthma or chronic bowel
CC   inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC   where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC   endocrine, motor or urogenital systems or skin are affected, and bone
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CC   marrow diseases. The products of the invention are chemokine derivatives
CC   which have cytostatic, antiinflammatory, antiasthmatic,
CC   immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC   Chemokines act on specific tumor and inflammatory cells through a
CC   constellation of chemokine receptors (CR), which control migration and
CC   proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC   fragments used to illustrate the method of the invention.
XX
SQ   Sequence   369 AA;


  Query Match            100.0%;  Score 1854;  DB 22;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-191;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
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Db      13 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 72

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
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Db     253 lkvtitvltvfvlsqfpyncillvqtidayamfisncavstnidicfqvtqtiaffhscl 312

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
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Db     313 npvlyvfvgerfrrdlvktlknlgcisqaqwvsftrregslklssmllettsgalsl 369


RESULT   5
AAY90649
ID   AAY90649 standard; Protein; 357 AA.
XX
AC   AAY90649;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human mutant G protein-coupled receptor GPR9-6 (L241K).
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   N-PSDB; AAA30715.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents -
XX
PS   Example 2; Page 226-227; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
CC   acids N-terminal of an endogenous proline in TM6 to form a sequence
CC   X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC   or Ala, and is preferably Lys. When the endogenous residue at this
CC   position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC   The 15 amino acid stretch between the substituted amino acid and the Pro
CC   may be endogenous, non-endogenous, or a mixture of endogenous and
CC   non-endogenous residues. The constitutively active GPCRs are useful for
CC   identifying antagonists, agonists and partial agonists for use as
CC   pharmaceutical agents. The mutant proteins are also useful in research
CC   settings for elucidating the roles of the receptors in normal and
CC   diseased conditions. Antagonists for a particular GPCR are useful for
CC   treating diseases and disorders associated with that receptor. Because
CC   the novel mutant GPCRs are constitutively active, they can be used
CC   directly for screening of compounds without the need for endogenous
CC   ligands. Sequences AAY90643- AAY90677 and AAY90683-Y90687 the mutant
CC   human GPCRs of the invention.
XX
SQ   Sequence   357 AA;


  Query Match            99.7%;  Score 1848;  DB 21;  Length 357;
  Best Local Similarity  99.7%;  Pred. No. 6.2e-191;
  Matches  356;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 60

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 ywyctrvktmtdmfllnlaiadllflvtlpfwaiaaadqwkfqtfmckvvnsmykmnfys 120

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 cvllimcisvdryiaiaqamrahtwrekrllyskmvcftiwvlaaalcipeilysqikee 180

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 sgiaictmvypsdestklksavltlkvilgfflpfvvmaccytiiihtliqakksskhka 240

Qy     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 kkvtitvltvfvlsqfpyncillvqtidayamfisncavstnidicfqvtqtiaffhscl 300

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 npvlyvfvgerfrrdlvktlknlgcisqaqwvsftrregslklssmllettsgalsl 357


RESULT   6
ABB56344
ID   ABB56344 standard; Protein; 369 AA.
XX
AC   ABB56344;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Non-endogenous human GPCR protein, SEQ ID NO: 481.
XX
KW   Human; G protein-coupled receptor; GPCR; non-endogenous; mutant;
KW   constitutively activated GPCR; agonist; disease.
```

XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200177172-A2.
XX
PD 18-OCT-2001.
XX
PF 05-APR-2001; 2001WO-US11098.
XX
PR 07-APR-2000; 2000US-195747P.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Lehmann-Bruinsma K, Liaw CW, Lin I;
XX
DR WPI; 2001-648759/74.
DR N-PSDB; ABI97980.
XX
PT Identifying agonists of G protein-coupled receptors (GPCRs) for use in
PT disease treatment, comprises contacting candidate compounds with
PT versions of GPCRs -
XX
PS Claim 1; Page 281-282; 394pp; English.
XX
CC The invention relates to G protein-coupled receptors (GPCRs) for which
CC the endogenous ligand has been identified. Non-endogenous
CC constitutively activated versions of known GPCRs are used in the
CC invention for the direct identification of candidate compounds as
CC receptor agonists, inverse agonists or partial agonists. Such
CC agonists are useful as therapeutic agents for diseases or disorders
CC associated with GPCRs. The present sequence is a non-endogenous
CC version of a known human GPCR.
XX
SQ Sequence 369 AA;

Query Match 99.7%; Score 1848; DB 22; Length 369;
Best Local Similarity 99.7%; Pred. No. 6.4e-191;
Matches 356; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      13 maddygsestssmedyvnfnftdfyceknnvrqfashflpplywlvfivgalgnslvilv 72

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      73 ywyctrvktmtdmfllnlaiadllflvtlpfwaiaaadqwkfqtfmckvvnsmykmnfys 132

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     133 cvllimcisvdryiaiaqamrahtwrekrllyskmvcftiwvlaaalcipeilysqikee 192

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     193 sgiaictmvypsdestklksavltlkvilgfflpfvvmaccytiiihtliqakkssknka 252

Qy     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     253 kkvtitvltvfvlsqfpyncillvqtidayamfisncavstnidicfqvtqtiaffhscl 312

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 npvlyvfvgerfrrdlvktlknlgcisqaqwvsftrregslklssmllettsgalsl 369
```

RESULT 7
AAR53745
ID AAR53745 standard; Protein; 358 AA.
XX
AC AAR53745;
XX
DT 02-FEB-1995 (first entry)
XX
DE Partial sequence of seven transmembrane receptor (V31).
XX
KW Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW polymerase chain reaction.
XX
OS Homo sapiens.
XX
PN WO9412635-A.
XX
PD 09-JUN-1994.
XX
PF 17-NOV-1993; 93WO-US11153.
XX
PR 17-NOV-1992; 92US-0977452.
XX
PA (ICOS-) ICOS CORP.
XX
PI Godiska R, Gray PW, Schweickart VL;
XX
DR WPI; 1994-200264/24.
DR N-PSDB; AAQ66162.
XX
PT DNA encoding seven trans:membrane receptors - used to develop
PT prods. for use as therapeutic or diagnostic agents for conditions
PT involving the receptors.
XX
PS Example 3; Page 56-57; 100pp; English.
XX
CC Two primers (AAQ66148, AAQ66149) were used to amplify human genomic DNA
CC purified from leukocytes. Approximately 1000 clones were isolated
CC after the intial amplification reation and probed with sequences
CC specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC Clones which did not hybridise were then chosen for sequence
CC analysis. Three new clones were identified that appeared to encode
CC seven transmembrane receptor segments. Two more primers (AAQ66151,
CC AAQ66152) were used to isolate a full length version of one of these
CC clones designated V31 (See AAQ66153). This is the sequence encoded
CC by exon 3 of the V31 genomic clone
XX
SQ Sequence 358 AA;

Query Match 42.1%; Score 780.5; DB 15; Length 358;
Best Local Similarity 42.9%; Pred. No. 1.2e-75;
Matches 153; Conservative 77; Mismatches 104; Indels 23; Gaps 6;

```
Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
             : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db       8 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 62

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db      63 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 122

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
            :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     123 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 182

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     183 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 236

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
            ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     237 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 296

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
             |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db     297 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 349
```

RESULT 8

```
AAB21689
ID   AAB21689 standard; Protein; 358 AA.
XX
AC   AAB21689;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Human 7TM receptor V31-B cDNA clone exon 1 protein.
XX
KW   Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW   G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   US6107475-A.
XX
PD   22-AUG-2000.
XX
PF   26-APR-1999;   99US-0299843.
XX
PR   17-MAY-1994;   94US-0245242.
PR   01-JUN-1998;   98US-0088337.
PR   17-NOV-1992;   92US-0977452.
PR   17-NOV-1993;   93US-0153848.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Schweickart VL,  Gray PW,  Godiska R;
XX
DR   WPI; 2000-571335/53.
DR   N-PSDB; AAA91709.
XX
PT   Polynucleotide encoding seven transmembrane receptors, antibody
PT   specific to the receptor, agonist and antagonist of the receptor useful
PT   for treating inflammation in a mammal  -
XX
PS   Example 3; Columns 49-52; 61pp; English.
XX
CC   The present sequence is a novel seven transmembrane (7TM) receptors
CC   (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC   The coding sequence for the present sequence may be used for gene
CC   therapy for diseases such as cancer.
XX
SQ   Sequence   358 AA;


  Query Match           42.1%;  Score 780.5;  DB 21;  Length 358;
  Best Local Similarity   42.9%;  Pred. No. 1.2e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db       8 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 62

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||||:|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db      63 yiyfkrlktmtdtyllnlavadilfltlpfwaysaakswvfgvhfcklifaiykmsffs 122

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     123 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 182

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     183 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 236

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
           ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     237 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 296

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
             |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db     297 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 349


RESULT   9
AAW48724
ID   AAW48724 standard; Protein; 378 AA.
XX
AC   AAW48724;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Human V31 seven transmembrane receptor.
XX
KW   V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
KW   immunology; inflammation; V31.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          58..86
FT                   /note= "Transmembrane domain 1"
FT   Domain          96..119
FT                   /note= "Transmembrane domain 2"
FT   Domain          131..152
FT                   /note= "Transmembrane domain 3"
FT   Domain          171..196
FT                   /note= "Transmembrane domain 4"
FT   Domain          219..247
FT                   /note= "Transmembrane domain 5"
FT   Domain          264..285
FT                   /note= "Transmembrane domain 6"
FT   Domain          306..331
FT                   /note= "Transmembrane domain 7"
XX
PN   US5759804-A.
XX
PD   02-JUN-1998.
XX
PF   17-NOV-1993;   93US-0153848.
XX
PR   17-NOV-1992;   92US-0977452.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Godiska R,  Gray PW,  Schweickart VL;
XX
DR   WPI; 1998-332132/29.
DR   N-PSDB; AAV18347.
XX
PT   DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT   for producing recombinant polypeptide and anti-V28 antibodies, and
PT   in screening assays for V28 agonists and antagonists
XX
PS   Example 3; Columns 39-42; 56pp; English.
XX
CC   The present sequence represents the V31 seven transmembrane (7TM)
CC   receptor encoded by the V31 cDNA (AAV18347).  The invention claims for
CC   a full length V28 genomic DNA (AAV18343) and the V28 protein it
CC   encodes (AAW48722).  V28  and V31 proteins are 7TM receptors which
CC   are probably involved in signal transduction.  The invention also
CC   claims that cells transformed with V28 DNA can be used to produce the
CC   recombinant polypeptide, to produce anti-V28 antibodies or in screening
CC   assays for V28 agonists or antagonists.  The antibodies, agonists and
CC   antagonists could then be used to modulate V28 receptor-ligand binding,
CC   for e.g. in immunological and/or inflammatory events in vivo.
XX
SQ   Sequence   378 AA;


  Query Match           42.1%;  Score 780.5;  DB 19;  Length 378;
  Best Local Similarity   42.9%;  Pred. No. 1.2e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;
```

```
Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
Db      28 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
Db      83 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
Db     143 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
Db     203 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 256

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
Db     257 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 316

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
Db     317 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 369


RESULT 10
AAB21688
ID   AAB21688 standard; Protein; 378 AA.
XX
AC   AAB21688;
XX
DT   26-JAN-2001  (first entry)
XX
DE   Human 7TM receptor V31-B cDNA clone protein.
XX
KW   Seven transmembrane receptor; 7TM; heptahelical; serpentine;
KW   G-protein-coupled; V28; V31; V112; R20; R2; R12; RM3; gene therapy;
KW   cancer.
XX
OS   Homo sapiens.
XX
PN   US6107475-A.
XX
PD   22-AUG-2000.
XX
PF   26-APR-1999;   99US-0299843.
XX
PR   17-MAY-1994;   94US-0245242.
PR   01-JUN-1998;   98US-0088337.
PR   17-NOV-1992;   92US-0977452.
PR   17-NOV-1993;   93US-0153848.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Schweickart VL,  Gray PW,  Godiska R;
XX
DR   WPI; 2000-571335/53.
DR   N-PSDB; AAA91707.
XX
PT   Polynucleotide encoding seven transmembrane receptors, antibody
PT   specific to the receptor, agonist and antagonist of the receptor useful
PT   for treating inflammation in a mammal  -
XX
PS   Example 3; Columns 41-44; 61pp; English.
XX
CC   The present sequence is a novel seven transmembrane (7TM) receptors
CC   (also known as heptahelical, serpentine or G-protein-coupled receptors).
CC   The coding sequence for the present sequence may be used for gene
CC   therapy for diseases such as cancer.
XX
SQ   Sequence   378 AA;
```

```
  Query Match           42.1%;  Score 780.5;  DB 21;  Length 378;
  Best Local Similarity   42.9%;  Pred. No. 1.2e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
Db      28 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
Db      83 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
Db     143 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
Db     203 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 256

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
Db     257 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 316

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
Db     317 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 369


RESULT 11
AAY90629
ID   AAY90629 standard; Protein; 378 AA.
XX
AC   AAY90629;
XX
DT   21-AUG-2000  (first entry)
XX
DE   Human G protein-coupled receptor EBI1.
XX
KW   G protein-coupled receptor; GPCR; constitutively active;
KW   intracellular loop 3; transmembrane domain 6; drug screening;
KW   agonist; antagonist.
XX
OS   Homo sapiens.
XX
PN   WO200022129-A1.
XX
PD   20-APR-2000.
XX
PF   12-OCT-1999;   99WO-US23938.
XX
PR   13-OCT-1998;   98US-0170496.
XX
PA   (AREN-) ARENA PHARM INC.
XX
PI   Behan DP,  Chalmers DT,  Liaw CW;
XX
DR   WPI; 2000-329165/28.
DR   N-PSDB; AAA30632.
XX
PT   Non-endogenous constitutively activated human G protein-coupled
PT   receptors, useful for identifying agonists for use as pharmaceutical
PT   agents  -
XX
PS   Example 1; Page 158-159; 341pp; English.
XX
CC   The invention relates to constitutively active, non-endogenous versions
CC   of endogenous human orphan G protein-coupled receptors (GPCRs, AAY90643-
CC   AAY90677 and AAY90683-Y90687), and to DNA encoding them (AAA30709-A30743
CC   and AAA30775-A30779). The mutant proteins of the invention contain a
CC   mutation in a portion of the protein comprising intracellular loop 3
CC   (IC3) and transmembrane domain 6 (TM6). A non-endogenous amino acid, X,
CC   is substituted for an endogenous residue in IC3 at a position 16 amino
```

CC acids N-terminal of an endogenous proline in TM6 to form a sequence
CC X-(AA)15-Pro. The endogenous amino acid is selected from Lys, His, Arg
CC or Ala, and is preferably Lys. When the endogenous residue at this
CC position is Lys, this residue is replaced by His, Arg or preferably Ala.
CC The 15 amino acid stretch between the substituted amino acid and the Pro
CC may be endogenous, non-endogenous, or a mixture of endogenous and
CC non-endogenous residues. The constitutively active GPCRs are useful for
CC identifying antagonists, agonists and partial agonists for use as
CC pharmaceutical agents. The mutant proteins are also useful in research
CC settings for elucidating the roles of the receptors in normal and
CC diseased conditions. Antagonists for a particular GPCR are useful for
CC treating diseases and disorders associated with that receptor. Because
CC the novel mutant GPCRs are constitutively active, they can be used
CC directly for screening of compounds without the need for endogenous
CC ligands. The present sequence represents a human wild-type GPCR referred
CC to in an exemplification of the invention.
XX
SQ Sequence 378 AA;

ery Match 42.1%; Score 780.5; DB 21; Length 378;
st Local Similarity 42.9%; Pred. No. 1.2e-75;
Matches 153; Conservative 77; Mismatches 104; Indels 23; Gaps 6;

```
Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db      28 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db      83 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     143 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     203 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 256

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
           ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     257 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 316

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
             |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db     317 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 369
```

LT 12
AAB80114
ID AAG80114 standard; Protein; 378 AA.
XX
AC AAG80114;
XX
DT 17-JAN-2002 (first entry)
XX
DE Human CCR7 protein.
XX
KW Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection;
KW inflammation; autoimmune disease; metastasis; bronchial asthma; lupus;
KW chronic bowel inflammation; rheumatoid arthritis; cytostatic;
KW antiinflammatory; antiasthmatic; immunosuppressive; dermatological;
KW antirheumatic; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200172830-A2.
XX
PD 04-OCT-2001.
XX
PF 02-APR-2001; 2001WO-EP03708.
XX
PR 31-MAR-2000; 2000DE-1016013.
XX
PA (IPFP-) IPF PHARM GMBH.
PA (FORS/) FORSSMANN U.
XX
PI Forssmann W, Adermann K, Heitland A, Spodsberg N;
XX
DR WPI; 2001-626256/72.
XX
PT Diagnostic agent containing two or more receptor-specific ligands,
PT useful for detecting tumors, inflammation etc., also therapeutic use of
PT ligand inhibitors -
XX
PS Disclosure; Page 10; 26pp; German.
XX
CC This invention describes a novel diagnostic agent (A) comprising at least
CC two different ligands (I) for receptors (II) that are implicated in
CC disease. (A) are used for the diagnosis of tumors (especially colorectal
CC or prostatic), organ rejection, inflammation and autoimmune diseases.
CC Also inhibitors of (I) are used therapeutically against tumors (and their
CC metastases), inflammation (particularly bronchial asthma or chronic bowel
CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
CC endocrine, motor or urogenital systems or skin are affected, and bone
CC marrow diseases. The products of the invention are chemokine derivatives
CC which have cytostatic, antiinflammatory, antiasthmatic,
CC immunosuppressive, dermatological, antirheumatic, antiarthritic.
CC Chemokines act on specific tumor and inflammatory cells through a
CC constellation of chemokine receptors (CR), which control migration and
CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
CC fragments used to illustrate the method of the invention.
XX
SQ Sequence 378 AA;

Query Match 42.1%; Score 780.5; DB 22; Length 378;
Best Local Similarity 42.9%; Pred. No. 1.2e-75;
Matches 153; Conservative 77; Mismatches 104; Indels 23; Gaps 6;

```
Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db      28 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db      83 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     143 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     203 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 256

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
           ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     257 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 316

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
             |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db     317 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 369
```

RESULT 13
AAB50859
ID AAB50859 standard; protein; 378 AA.
XX
AC AAB50859;
XX
DT 16-MAR-2001 (first entry)
XX
DE Human CCR7.

```
XX
KW   Human; chemokine receptor 7; CCR7; chemokine beta-9; CKbeta-9;
KW   allergy; autoimmune disease; ischaemia; atherosclerosis; cancer;
KW   chronic inflammatory disorder; organ transplant; tissue graft;
KW   chronic myelogenous leukaemia; infection.
XX
OS   Homo sapiens.
XX
PN   US6153441-A.
XX
PD   28-NOV-2000.
XX
PF   17-FEB-1999;   99US-0251545.
XX
PR   17-FEB-1998;   98US-0074883.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Appelbaum ER,  White JR,  Sarau HM;
XX
DR   WPI; 2001-049151/06.
XX
PT   Identifying agonists or antagonists of interaction between human
PT   protein, chemokine beta-9 and human CC chemokine receptor 7, by
PT   contacting cell expressing receptor with test compound -
XX
PS   Claim 1; Fig 1; 20pp; English.
XX
CC   The present sequence is human chemokine receptor 7 (CCR7), a cellular
CC   receptor for chemokine beta-9 (CKbeta-9). The sequence may be
CC   used in a method for discovering agonists and antagonists of the
CC   interaction between CKbeta-9 and CCR7. A cell expressing CCR7
CC   polypeptide on its surface, associated with a component capable of
CC   providing a detectable signal in response to binding of CKbeta-9, is
CC   contacted with a compound in the presence of labelled or unlabelled
CC   CKbeta-9. The compound is identified as an agonist/antagonist by
CC   determining whether it activates or inhibits the detectable signal.
CC   The method is useful for identifying agonists and antagonists of the
CC   interaction between CKbeta-9 and CCR7 which are useful for treating
CC   diseases including allergic disorders, autoimmune diseases,
CC   ischaemia/reperfusion injury, development of atherosclerotic plaques,
CC   cancer, chronic inflammatory disorders, chronic rejection of
CC   transplanted organs or tissue grafts, chronic myelogenous leukaemia, and
CC   infection by HIV and other pathogens.
XX
SQ   Sequence   378 AA;

  Query Match             42.1%;  Score 780.5;  DB 22;  Length 378;
  Best Local Similarity   42.9%;  Pred. No. 1.2e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db      28 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db      83 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
            :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     143 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     203 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 256

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
            ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     257 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 316

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
                |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db     317 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 369


RESULT  14
AAR53743
ID   AAR53743 standard; Protein; 410 AA.
XX
AC   AAR53743;
XX
DT   02-FEB-1995  (first entry)
XX
DE   Putative seven transmembrane receptor (V31).
XX
KW   Primer; seven transmembrane receptor; receptor; amplification; PCR;
KW   polymerase chain reaction.
XX
OS   Homo sapiens.
XX
PN   WO9412635-A.
XX
PD   09-JUN-1994.
XX
PF   17-NOV-1993;   93WO-US11153.
XX
PR   17-NOV-1992;   92US-0977452.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Godiska R,  Gray PW,  Schweickart VL;
XX
DR   WPI; 1994-200264/24.
DR   N-PSDB; AAQ66153.
XX
PT   DNA encoding seven trans:membrane receptors - used to develop
PT   prods. for use as therapeutic or diagnostic agents for conditions
PT   involving the receptors.
XX
PS   Example 2; Page 46-48; 100pp; English.
XX
CC   Two primers (AAQ66148, AAQ66149) were used to amplify human genomic DNA
CC   purified from leukocytes.  Approximately 1000 clones were isolated
CC   after the intial amplification reation and probed with sequences
CC   specific for seven transmembrane receptors IL8R1, AT2R and R20.
CC   Clones which did not hybridise were then chosen for sequence
CC   analysis.  Three new clones were identified that appeared to encode
CC   seven transmembrane receptor segments.  Two more primers (AAQ66151,
CC   AAQ66152) were used to isolate a full length version of one of these
CC   clones, one of which was designated V31 and encoded this
CC   polypeptide.
XX
SQ   Sequence   410 AA;

  Query Match             42.1%;  Score 780.5;  DB 15;  Length 410;
  Best Local Similarity   42.9%;  Pred. No. 1.4e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db      60 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 114

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db     115 yiyfkrlktmtdtyllnlavadilflltlpfwaysaakswvfgvhfcklifaiykmsffs 174

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
            :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     175 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 234

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     235 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 288
```

```
Qy    236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
          ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db    289 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 348

Qy    296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
            |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db    349 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 401


RESULT 15
AAW48723
ID   AAW48723 standard; Protein; 410 AA.
XX
AC   AAW48723;
XX
DT   25-SEP-1998  (first entry)
XX
DE   Polypeptide sequence encoded by the human V31 genomic DNA.
XX
K    V28; placenta; seven transmembrane receptor; 7TM; signal transduction;
K    immunology; inflammation; V31.
XX
OS   Homo sapiens.
XX
PN   US5759804-A.
XX
PD   02-JUN-1998.
XX
PF   17-NOV-1993;   93US-0153848.
XX
PR   17-NOV-1992;   92US-0977452.
XX
PA   (ICOS-) ICOS CORP.
XX
PI   Godiska R,  Gray PW,  Schweickart VL;
XX
DR   WPI; 1998-332132/29.
DR   N-PSDB; AAV18345.
XX
PT   DNA encoding V28 seven transmembrane receptor polypeptide - useful
PT   for producing recombinant polypeptide and anti-V28 antibodies, and
PT   in screening assays for V28 agonists and antagonists
XX
PS   Example 2; Columns 31-34; 56pp; English.
XX
CC   The present sequence represents the deduced polypeptide sequence encoded
CC   by the V31 genomic DNA (AAV18345) which was isolated from a human
CC   placenta genomic library.  The invention claims for a full length V28
CC   genomic DNA (AAV18343) and the V28 (AAW48722) protein it encodes.  V28
CC   and V31 (AAW48723) proteins are seven transmembrane (7TM) receptors which
CC   are probably involved in signal transduction.  The invention also claims
CC   that cells transformed with V28 DNA can be used to produce the
CC   recombinant polypeptide, to produce anti-V28 antibodies or in screening
CC   assays for V28 agonists or antagonists. The antibodies, agonists and
CC   antagonists could then be used to modulate V28 receptor-ligand binding,
CC   for e.g. in immunological and/or inflammatory events in vivo.
XX
SQ   Sequence   410 AA;


  Query Match             42.1%;  Score 780.5;  DB 19;  Length 410;
  Best Local Similarity   42.9%;  Pred. No. 1.4e-75;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy      1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
          : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db     60 vtddyigdntt-----vdytlfeslcskkdvrnfkawflpimysiicfvgllgnglvvlt 114

Qy     61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
          | |  |:|||| :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
Db    115 yiyfkrlktmtdtyllnlavadilfltlpfwaysaakswvfgvhfcklifaiykmsffs 174

Qy    121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
          :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db    175 gmllllcisidryvaivqavsahrhrarvllisklscvgiwilatvlsipellysdlqrs 234

Qy    181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
          |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db    235 sseqamrcsli------tehveafitiqvaqmvigflvpllamsfcylviirtllqarnf 288

Qy    236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
          ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db    289 ernkaikviiavvvvfivfqlpyngvvlaqtvanfnitsstcelskqlniaydvtyslac 348

Qy    296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
            |:|| || |:| :|| || |  |:|||:||    || |       :: ||| :|
Db    349 vrccvnpflyafigvkfrndlfklfkdlgclsqeqlrqwsscrh----irrssmsve 401


Search completed: October  1, 2002, 06:29:34
Job time: 319 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 1, 2002, 06:26:10 ; Search time 12.97 Seconds
(without alignments)
672.316 Million cell updates/sec

Title: US-09-522-752-2
Perfect score: 1854
Sequence: 1 MADDYGSESTSSMEDYVNFN.....EGSLKLSSMLLETTSGALSL 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1854	100.0	357	4	US-09-266-464-2	Sequence 2, Appli
2	780.5	42.1	358	1	US-08-153-848-19	Sequence 19, Appl
3	780.5	42.1	358	3	US-09-299-843A-19	Sequence 19, Appl
4	780.5	42.1	358	4	US-09-088-337B-19	Sequence 19, Appl
5	780.5	42.1	358	5	PCT-US93-11153-19	Sequence 19, Appl
6	780.5	42.1	378	1	US-08-153-848-15	Sequence 15, Appl
7	780.5	42.1	378	3	US-09-299-843A-15	Sequence 15, Appl
8	780.5	42.1	378	4	US-09-251-545-1	Sequence 1, Appli
9	780.5	42.1	378	4	US-09-088-337B-15	Sequence 15, Appl
10	780.5	42.1	378	5	PCT-US93-11153-15	Sequence 15, Appl
11	780.5	42.1	410	1	US-08-153-848-7	Sequence 7, Appli
12	780.5	42.1	410	3	US-09-299-843A-7	Sequence 7, Appli
13	780.5	42.1	410	4	US-09-088-337B-7	Sequence 7, Appli
14	780.5	42.1	410	5	PCT-US93-11153-7	Sequence 7, Appli
15	758.5	40.9	378	1	US-08-383-750-2	Sequence 2, Appli
16	758.5	40.9	378	1	US-08-383-751A-2	Sequence 2, Appli
17	758.5	40.9	378	3	US-08-352-678-2	Sequence 2, Appli
18	758.5	40.9	378	4	US-09-045-583-49	Sequence 49, Appl
19	758.5	40.9	378	5	PCT-US93-09636-2	Sequence 2, Appli
20	757.5	40.9	378	3	US-09-299-843A-66	Sequence 66, Appl
21	757.5	40.9	378	4	US-09-088-337B-66	Sequence 66, Appl
22	742	40.0	359	1	US-08-153-848-24	Sequence 24, Appl
23	742	40.0	359	3	US-09-299-843A-24	Sequence 24, Appl
24	742	40.0	359	4	US-09-088-337B-24	Sequence 24, Appl
25	742	40.0	359	5	PCT-US93-11153-24	Sequence 24, Appl
26	721	38.9	361	2	US-08-902-294-2	Sequence 2, Appli
27	721	38.9	361	3	US-09-178-637-2	Sequence 2, Appli
28	652	35.2	350	2	US-08-966-316-18	Sequence 18, Appl
29	638.5	34.4	374	4	US-09-045-583-48	Sequence 48, Appl
30	637	34.4	350	2	US-08-966-316-16	Sequence 16, Appl
31	624	33.7	342	4	US-09-116-498-6	Sequence 6, Appli
32	619	33.4	342	4	US-09-116-498-4	Sequence 4, Appli
33	612	33.0	342	2	US-08-742-011-2	Sequence 2, Appli
34	612	33.0	342	4	US-09-275-384B-5	Sequence 5, Appli
35	612	33.0	342	4	US-09-116-498-2	Sequence 2, Appli
36	612	33.0	342	4	US-09-449-437A-2	Sequence 2, Appli
37	598	32.3	352	4	US-09-045-583-52	Sequence 52, Appl
38	596	32.1	352	4	US-09-087-232A-13	Sequence 13, Appl
39	596	32.1	352	4	US-08-861-105-14	Sequence 14, Appl
40	596	32.1	352	4	US-08-575-967A-2	Sequence 2, Appli
41	590	31.8	352	3	US-08-466-343D-2	Sequence 2, Appli
42	585.5	31.6	360	4	US-08-875-573-20	Sequence 20, Appl
43	585.5	31.6	360	4	US-09-232-878-2	Sequence 2, Appli
44	585.5	31.6	360	4	US-09-045-583-55	Sequence 55, Appl
45	582	31.4	360	1	US-08-202-056-7	Sequence 7, Appli

ALIGNMENTS

```
RESULT 1
US-09-266-464-2
; Sequence 2, Application US/09266464
; GENERAL INFORMATION:
; APPLICANT: Andrew, David P.
; APPLICANT: Zabel, Brian A.
; APPLICANT: Ponath, Paul D.
; TITLE OF INVENTION: ANTI-GPR-9-6 ANTIBODIES AND METHODS OF
; TITLE OF INVENTION: IDENTIFYING AGENTS WHICH MODULATE GPR-9-6 FUNCTION
; FILE REFERENCE: LKS98-16
; CURRENT APPLICATION NUMBER: US/09/266,464
; CURRENT FILING DATE: 1999-03-11
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-266-464-2

  Query Match            100.0%;  Score 1854;  DB 4;  Length 357;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-162;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240

Qy     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
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RESULT   2
US-08-153-848-19
; Sequence 19, Application US/08153848
; Patent No. 5759804
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 5759804el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  64
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/153,848
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5759804and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31794
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  358 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-153-848-19


  Query Match           42.1%;  Score 780.5;  DB 1;  Length 358;
  Best Local Similarity   42.9%;  Pred. No. 8.8e-64;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db       8 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLT 62

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Db      63 YIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFS 122

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     123 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQRS 182

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |    |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     183 SSEQAMRCSLI------TEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNF 236

Qy     236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
           ::||:|| | |: ||:: | ||| ::| ||:  : :  | | :|  ::| : || ::|
Db     237 ERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLAC 296

Qy     296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
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RESULT   3
US-09-299-843A-19
; Sequence 19, Application US/09299843A
; Patent No. 6107475
;  GENERAL INFORMATION:
;    APPLICANT:  Godiska, Ronald
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Schweikart, Vicki L.
;    TITLE OF INVENTION:  No. 6107475el Seven Transmembrane Receptors
;    NUMBER OF SEQUENCES:  66
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/299,843A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/088,337
;      FILING DATE:  01-JUN-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/153,848
;      FILING DATE:  17-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,452
;      FILING DATE:  17-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jill E. Uhl
;      REGISTRATION NUMBER:  43,213
;      REFERENCE/DOCKET NUMBER:  27866/32059B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  19:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  358 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-299-843A-19


  Query Match           42.1%;  Score 780.5;  DB 3;  Length 358;
  Best Local Similarity   42.9%;  Pred. No. 8.8e-64;
  Matches  153;  Conservative   77;  Mismatches  104;  Indels   23;  Gaps    6;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
           : |||  ::|:     |::   :  | | :|| | : ||| :| ::  || ||| ||:|
Db       8 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLT 62

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
             | |  |:|||||  :|||||:||:|||:|||||| :||  | |    ||:: ::|||:|:|
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Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
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Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 1, 2002, 06:26:30 ; Search time 46.91 Seconds
(without alignments)
731.270 Million cell updates/sec

Title: US-09-522-752-2
Perfect score: 1854
Sequence: 1 MADDYGSESTSSMEDYVNFN.....EGSLKLSSMLLETTSGALSL 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	780.5	42.1	378	2	B55735	lymphocyte-specifi
2	758.5	40.9	378	2	A45680	G protein-coupled
3	757.5	40.9	378	2	A55735	G protein-coupled
4	652	35.2	350	2	JN0621	G protein-coupled
5	638.5	34.4	369	2	JC5068	G protein-coupled
6	596	32.1	352	2	A43113	chemokine (C-C) re
7	585.5	31.6	360	2	A57160	chemokine (C-C) re
8	582	31.4	360	2	A53611	interleukin-8 rece
9	577	31.1	360	2	JC4587	chemokine (C-C) re
10	575	31.0	360	2	JC2443	chemokine (C-C) re
11	571	30.8	355	2	A45177	chemokine (C-C) re
12	569	30.7	374	2	I38450	chemokine (C-C) re
13	569	30.7	383	2	S55594	G protein-coupled
14	566	30.5	358	2	A53752	interleukin-8 rece
15	565.5	30.5	353	2	S28787	neuropeptide Y/pep
16	560	30.2	355	2	G02436	chemokine (C-C) re
17	558.5	30.1	350	2	A39445	interleukin-8 rece
18	558.5	30.1	355	2	JQ1231	interleukin-8 rece
19	557.5	30.1	352	2	A45747	neuropeptide Y/pep
20	555	29.9	359	2	I49341	MIP-1 alpha recept
21	547.5	29.5	352	2	G00048	fusin (LESTRA) - c
22	545	29.4	359	2	A48921	interleukin-8 rece
23	543.5	29.3	356	2	S42096	interleukin-8 rece
24	528	28.5	374	2	S32785	G protein-coupled
25	527.5	28.5	355	2	I49339	macrophage inflamm
26	526.5	28.4	374	2	S42628	G protein-coupled
27	524	28.3	327	2	S56162	MDCR15 protein - h
28	521.5	28.1	359	2	S15403	angiotensin II rec
29	521.5	28.1	372	2	S26667	G protein-coupled
30	517.5	27.9	359	2	S44425	angiotensin II rec
31	516.5	27.9	359	2	JC1104	angiotensin II rec
32	512	27.6	355	2	JC5067	G protein-coupled
33	512	27.6	367	2	JE0349	interferon-inducib
34	508.5	27.4	359	2	A48857	angiotensin II rec
35	505.5	27.3	359	2	A42656	angiotensin II rec
36	504.5	27.2	359	2	I39418	angiotensin II rec
37	504.5	27.2	359	2	JC2134	angiotensin II rec
38	501.5	27.0	359	2	JC1194	angiotensin II rec
39	500	27.0	356	2	I49340	MIP-1 alpha recept
40	498.5	26.9	359	2	JH0621	angiotensin II rec
41	494.5	26.7	359	2	JQ1516	angiotensin II rec
42	491.5	26.5	362	2	JN0694	angiotensin II rec
43	483	26.1	354	2	A23669	interleukin-8 rece
44	482.5	26.0	355	2	JC4304	orphan G protein-c
45	479	25.8	354	2	B55733	G protein-coupled

ALIGNMENTS

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lymphocyte-specific G protein-coupled receptor EBI1 - human
N;Alternate names: Burkitt's lymphoma receptor 2; Epstein-Barr virus induced protein
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B55735; S52443
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled recep
A;Reference number: A55735; MUID:95154835
A;Accession: B55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31581; NID:g468319; PIDN:AAA74231.1; PID:g468320
R;Burgstahler, R.; Kempkes, B.; Staeube, K.; Lipp, M.
submitted to the EMBL Data Library, February 1995
A;Description: The expression of the chemokine receptor BLR2/EBI1 is specifically tra
A;Reference number: S52443
A;Accession: S52443
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 21-378 <BUR>
A;Cross-references: EMBL:X84702
C;Genetics:
A;Gene: GDB:CMKBR7; EBI1; BLR2; CCR7
A;Cross-references: GDB:342065; OMIM:600242
A;Map position: 17q12-17q21.2
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor

Query Match 42.1%; Score 780.5; DB 2; Length 378;
Best Local Similarity 42.9%; Pred. No. 3.9e-60;
Matches 153; Conservative 77; Mismatches 104; Indels 23; Gaps 6;

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Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
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Db      28 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLT 82

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Db      83 YIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFS 142

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
           :||::|||:|||:|| ||: ||  | : || ||: |  ||:||  | |||:||| ::
Db     143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGIWILATVLSIPELLYSDLQRS 202

Qy     181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
           |      |:::      |:   | :|::|   ::|| :| : |: || :|| ||:||:
Db     203 SSEQAMRCSLI------TEHVEAFITIQVAQMVIGFLVPLLAMSFCYLVIIRTLLQARNF 256
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G protein-coupled peptide receptor EBI 1 - human
C;Species: Homo sapiens (man)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 24-Nov-1999
C;Accession: A45680
R;Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Lenoir, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A;Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled p
A;Reference number: A45680; MUID:93188173
A;Accession: A45680
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-378 <BIR>
A;Cross-references: GB:L08176; NID:g183484; PID:g183485
A;Experimental source: B-lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:127094, NCBIP:127095)
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; transmembrane protein


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  Best Local Similarity   42.0%;  Pred. No. 3.1e-58;
  Matches  150;  Conservative   78;  Mismatches  106;  Indels   23;  Gaps    6;

Qy      1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
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Db     28 VTDDYIGDNTT-----VDYTLFESLCSKKDVRNFKAWFLPIMYSIICFVGLLGNGLVVLT 82

Qy     61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
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Db     83 YIYFKRLKTMTDTYLLNLAVADILFLLTLPFWAYSAAKSWVFGVHFCKLIFAIYKMSFFS 142

Qy    121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
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Db    143 GMLLLLCISIDRYVAIVQAVSAHRHRARVLLISKLSCVGSAILATVLSIPELLYSDLQRS 202

Qy    181 SG--IAICTMVYPSDESTKLKSAVLTLKV---ILGFFLPFVVMACCYTIIIHTLIQAKKS 235
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Db    257 ERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITSSTCELSKQLNIAYDVTYSLAC 316

Qy    296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQ---AQWVSFTRREGSLKLSSMLLE 349
            |:|| || |:| :|| |: |  |:|||:||    || |       :: ||| :|
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RESULT   3
A55735
G protein-coupled receptor EBI1 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Nov-1999
C;Accession: A55735
R;Schweickart, V.L.; Raport, C.J.; Godiska, R.; Byers, M.G.; Eddy Jr., R.L.; Shows, T.B.
Genomics 23, 643-650, 1994
A;Title: Cloning of human and mouse EBI1, a lymphoid-specific G-protein-coupled receptor
A;Reference number: A55735; MUID:95154835
A;Accession: A55735
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-378 <SCH>
A;Cross-references: GB:L31580; NID:g468340; PIDN:AAA74232.1; PID:g468341
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor


  Query Match             40.9%;  Score 757.5;  DB 2;  Length 378;
  Best Local Similarity   43.2%;  Pred. No. 3.8e-58;
  Matches  156;  Conservative   74;  Mismatches  108;  Indels   23;  Gaps    7;

Qy      1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
          : |||  |:|:     |::   :  | | :|| | : ||| :| ::  || ||| ||||
Db     28 VTDDYIGENTT-----VDYTLYESVCFKKDVRNFKAWFLPLMYSVICFVGLLGNGLVILT 82

Qy     61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
          | |  |:|||| :|||||:||:|||: |||||  : |  | |  ::|| :  :|||::|:|
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Qy    236 SKHKALKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAF 295
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Db    257 ERNKAIKVIIAVVVVFIVFQLPYNGVVLAQTVANFNITNSSCETSKQLNIAYDVTYSLAS 316

Qy    296 FHSCLNPVLYVFVGERFRRDLVKTLKNLGCISQAQ---WVSFTR-REGSLKLSSMLLETT 351
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Db    317 VRCCVNPFLYAFIGVKFRSDLFKLFKDLGCLSQERLRHWSSCRHVRNASV---SMEAETT 373

Qy    352 S 352
          :
Db    374 T 374


RESULT   4
JN0621
G protein-coupled receptor type B - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 19-May-2000
C;Accession: JN0621
R;Matsuoka, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993
A;Title: Identification of novel members of G-protein coupled receptor superfamily ex
A;Reference number: JN0621; MUID:93326166
A;Accession: JN0621
A;Molecule type: mRNA
A;Residues: 1-350 <MAT>
A;Cross-references: GB:S63848; NID:g399710; PIDN:AAB27547.1; PID:g399711
A;Experimental source: tongue taste papillae
C;Comment: This protein is involved in modulating taste sensitivity or regeneration o
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein
F;42-66/Domain: transmembrane #status predicted <TM1>
F;80-99/Domain: transmembrane #status predicted <TM2>
F;114-135/Domain: transmembrane #status predicted <TM3>
F;154-175/Domain: transmembrane #status predicted <TM4>
F;200-222/Domain: transmembrane #status predicted <TM5>
F;242-265/Domain: transmembrane #status predicted <TM6>
F;284-306/Domain: transmembrane #status predicted <TM7>
F;6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted


  Query Match             35.2%;  Score 652;  DB 2;  Length 350;
  Best Local Similarity   37.9%;  Pred. No. 5e-49;
  Matches  127;  Conservative   70;  Mismatches  114;  Indels   24;  Gaps    5;

Qy      1 MADDYGSEST------SSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGN 54
          || :| ::||      : | |  :::  :  | |  ||:||  |||  : : ||:|  ||
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 1, 2002, 06:29:56 ; Search time 13.53 Seconds
(without alignments)
1021.647 Million cell updates/sec

Title: US-09-522-752-2
Perfect score: 1854
Sequence: 1 MADDYGSESTSSMEDYVNFN.....EGSLKLSSMLLETTSGALSL 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1854	100.0	357	1	CKR9_HUMAN	P51686 homo sapien
2	1642	88.6	369	1	CKR9_MOUSE	Q9wut7 mus musculu
3	780.5	42.1	378	1	CKR7_HUMAN	P32248 homo sapien
4	757.5	40.9	378	1	CKR7_MOUSE	P47774 mus musculu
5	652	35.2	350	1	CKRB_BOVIN	P35350 bos taurus
6	638.5	34.4	374	1	CKR6_HUMAN	P51684 homo sapien
7	637	34.4	350	1	CKRB_HUMAN	Q9npb9 homo sapien
8	624	33.7	342	1	CCR6_MACNE	O19024 macaca neme
9	619	33.4	342	1	CCR6_CERAE	O18983 cercopithec
10	617	33.3	343	1	CCR6_MACMU	Q9xt45 macaca mula
11	612	33.0	342	1	CCR6_HUMAN	O00574 homo sapien
12	606	32.7	352	1	CKR5_CERTO	O62743 cercocebus
13	605	32.6	367	1	CKR6_MOUSE	O54689 mus musculu
14	604	32.6	352	1	CKR5_CERAE	P56493 cercopithec
15	604	32.6	352	1	CKR5_GORGO	P56439 gorilla gor
16	603	32.5	352	1	CKR5_MACMU	P79436 macaca mula
17	602	32.5	352	1	CKR5_PAPHA	P56441 papio hamad
18	601	32.4	352	1	CKR5_PONPY	O97881 pongo pygma
19	598	32.3	352	1	CKR5_PANTR	P56440 pan troglod
20	598	32.3	352	1	CKR5_TRAFR	O97878 trachypithe
21	598	32.3	352	1	CKR5_TRAPH	O97879 trachypithe
22	597	32.2	352	1	CKR5_PYGBI	O97880 pygathrix b
23	597	32.2	352	1	CKR5_PYGNE	O97882 pygathrix n
24	596	32.1	352	1	CKR5_HUMAN	P51681 homo sapien
25	595	32.1	352	1	CKR5_HYLLE	O97883 hylobates l
26	585.5	31.6	354	1	CKR5_MOUSE	P51682 mus musculu
27	585.5	31.6	360	1	CKR4_HUMAN	P51679 homo sapien
28	582	31.4	360	1	IL8B_HUMAN	P25025 homo sapien
29	578	31.2	373	1	CKR2_RAT	O55193 rattus norv
30	577	31.1	360	1	CKR4_MOUSE	P51680 mus musculu
31	575	31.0	373	1	CKR2_MOUSE	P51683 mus musculu
32	573.5	30.9	354	1	CKR5_RAT	O08556 rattus norv
33	573	30.9	360	1	CKR2_MACMU	O18793 macaca mula
34	571	30.8	355	1	CKR1_HUMAN	P32246 homo sapien
35	570.5	30.8	353	1	IL8B_PANTR	Q28807 pan troglod
36	569.5	30.7	353	1	CCR4_FELCA	P56498 felis silve
37	569	30.7	374	1	CKR2_HUMAN	P41597 homo sapien
38	568.5	30.7	353	1	IL8B_MACMU	Q28519 macaca mula
39	566	30.5	358	1	IL8B_RABIT	P35344 oryctolagus
40	565.5	30.5	353	1	CCR4_BOVIN	P25930 bos taurus
41	565.5	30.5	353	1	IL8B_GORGO	Q28422 gorilla gor
42	564.5	30.4	350	1	IL8A_GORGO	P55919 gorilla gor
43	563	30.4	355	1	CKR3_HUMAN	P51677 homo sapien
44	558.5	30.1	350	1	IL8A_PANTR	P55920 pan troglod
45	558.5	30.1	355	1	IL8A_RABIT	P21109 oryctolagus

ALIGNMENTS

```
RESULT   1
CKR9_HUMAN
ID   CKR9_HUMAN     STANDARD;      PRT;   357 AA.
AC   P51686;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9) (GPR-9-
DE   6).
GN   CCR9 OR CMKBR9.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lautens L.L., Tiffany H.L., Gao J.-L., Modi W., Murphy P.M.,
RA   Bonner T.I.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   CHARACTERIZATION.
RX   MEDLINE=99248139; PubMed=10229797;
RA   Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT   "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
RT   as CCR9, the receptor for the chemokine TECK.";
RL   J. Immunol. 162:5671-5675(1999).
CC   -!- FUNCTION: Receptor for chemokine SCYA25/TECK. Subsequently
CC       transduces a signal by increasing the intracellular calcium ions
CC       level. Alternative coreceptor with CD4 for HIV-1 infection.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC       LYMPH NODES AND SPLEEN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U45982; AAA93319.1; -.
DR   GCRDb; GCR_1943; -.
DR   MIM; 604738; -.
DR   InterPro; IPR004069; Chemokine9_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01531; CHEMOKINER9.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN        1     37       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     38     64       1 (POTENTIAL).
FT   DOMAIN       65     73       CYTOPLASMIC (POTENTIAL).
```

```
FT   TRANSMEM     74     94       2 (POTENTIAL).
FT   DOMAIN       95    108       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    109    130       3 (POTENTIAL).
FT   DOMAIN      131    148       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    149    169       4 (POTENTIAL).
FT   DOMAIN      170    198       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    199    226       5 (POTENTIAL).
FT   DOMAIN      227    242       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    243    268       6 (POTENTIAL).
FT   DOMAIN      269    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    310       7 (POTENTIAL).
FT   DOMAIN      311    357       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD     20     20       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID    107    186       BY SIMILARITY.
SQ   SEQUENCE   357 AA;  40713 MW;  96982E0B922F6B31 CRC64;


  Query Match           100.0%;  Score 1854;  DB 1;  Length 357;
  Best Local Similarity  100.0%;  Pred. No. 6.3e-115;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240

Qy     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357


RESULT   2
CKR9_MOUSE
ID   CKR9_MOUSE     STANDARD;      PRT;   369 AA.
AC   Q9WUT7;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   C-C chemokine receptor type 9 (C-C CKR-9) (CC-CKR-9) (CCR-9)
DE   (Chemokine C-C receptor 10).
GN   CCR9 OR CMKBR10.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Thymus;
RX   MEDLINE=99248139; PubMed=10229797;
RA   Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT   "Cutting edge: identification of the orphan chemokine receptor GPR-9-6
RT   as CCR9, the receptor for the chemokine TECK.";
RL   J. Immunol. 162:5671-5675(1999).
CC   -!- FUNCTION: RECEPTOR FOR CHEMOKINE SCYA25/TECK. SUBSEQUENTLY
CC       TRANSDUCES A SIGNAL BY INCREASING THE INTRACELLULAR CALCIUM IONS
CC       LEVEL.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE THYMUS AND LOW IN
CC       LYMPH NODES AND SPLEEN.
CC   -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ132336; CAB43480.1; -.
DR   MGD; MGI:1341902; Cmkbr10.
DR   InterPro; IPR004069; Chemokine9_receptor.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR01531; CHEMOKINER9.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   G-protein coupled receptor; Transmembrane; Glycoprotein.
FT   DOMAIN       1     49       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    50     76       1 (POTENTIAL).
FT   DOMAIN      77     85       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    86    106       2 (POTENTIAL).
FT   DOMAIN     107    120       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   121    142       3 (POTENTIAL).
FT   DOMAIN     143    160       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   161    181       4 (POTENTIAL).
FT   DOMAIN     182    210       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   211    238       5 (POTENTIAL).
FT   DOMAIN     239    254       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM   255    280       6 (POTENTIAL).
FT   DOMAIN     281    304       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   305    322       7 (POTENTIAL).
FT   DOMAIN     323    369       CYTOPLASMIC (POTENTIAL).
FT   CARBOHYD    32     32       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DISULFID   119    198       BY SIMILARITY.
SQ   SEQUENCE   369 AA;  41913 MW;  6971F76F0A24B4AE CRC64;


  Query Match           88.6%;  Score 1642;  DB 1;  Length 369;
  Best Local Similarity  86.6%;  Pred. No. 4.9e-101;
  Matches  309;  Conservative   21;  Mismatches   27;  Indels    0;  Gaps    0;

Qy       1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
             | ||:  :||:| :||:| ||: |:|:|||||||||||||||||||||| ||||||||
Db      13 MFDDFSYDSTASTDDYMNLNFSSFFCKKNNVRQFASHFLPPLYWLVFIVGTLGNSLVILV 72

Qy      61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
             |||||||||||||||||||||||| |||||||||| || ||||||||||||||||||||
Db      73 YWYCTRVKTMTDMFLLNLAIADLLFLATLPFWAIAAAGQWMFQTFMCKVVNSMYKMNFYS 132

Qy     121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
             |||||||||||||||| |||:|  ||:|||||||||| ||||:|| || |||||||:  |
Db     133 CVLLIMCISVDRYIAIVQAMKAQVWRQKRLLYSKMVCITIWVMAAVLCTPEILYSQVSGE 192

Qy     181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
             |||| |||||| |:: ||||||| ||| |||||||:||| |||||||||:||||||||||
Db     193 SGIATCTMVYPKDKNAKLKSAVLILKVTLGFFLPFMVMAFCYTIIIHTLVQAKKSSKHKA 252

Qy     241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
             ||||||||||::|||||| ||:|| :|||||||||| :|||||||||||||||||||||
Db     253 LKVTITVLTVFIMSQFPYNSILVVQAVDAYAMFISNCTISTNIDICFQVTQTIAFFHSCL 312

Qy     301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     313 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 369


RESULT   3
CKR7_HUMAN
ID   CKR7_HUMAN     STANDARD;      PRT;   378 AA.
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: October 1, 2002, 06:28:56 ; Search time 28.28 Seconds
(without alignments)
2183.847 Million cell updates/sec

Title: US-09-522-752-2
Perfect score: 1854
Sequence: 1 MADDYGSESTSSMEDYVNFN.....EGSLKLSSMLLETTSGALSL 357

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Expected. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1854	100.0	369	4	Q9UQQ6	Q9uqq6 homo sapien
2	776.5	41.9	368	13	O42444	O42444 oncorhynchu
3	671.5	36.2	351	11	Q9EQ16	Q9eq16 mus musculu
4	665.5	35.9	351	11	Q9ERH5	Q9erh5 mus musculu
5	645	34.8	350	11	Q924I3	Q924i3 mus musculu
6	621	33.5	343	6	Q9N0Z0	Q9n0z0 cercocebus
7	616	33.2	342	6	Q9TV16	Q9tv16 pan troglod
8	616	33.2	352	6	Q9TV44	Q9tv44 cercopithec
9	614	33.1	367	11	Q9R1V0	Q9r1v0 mus musculu
10	613	33.1	343	6	Q9BDS6	Q9bds6 macaca fasc
11	612	33.0	342	4	Q9HCA5	Q9hca5 homo sapien
12	612	33.0	352	6	Q9XT76	Q9xt76 cercopithec
13	612	33.0	352	6	Q95ND1	Q95nd1 mandrillus
14	611	33.0	352	6	Q9BGN6	Q9bgn6 cercopithec
15	608	32.8	352	6	Q95ND2	Q95nd2 mandrillus
16	607	32.7	352	6	Q9TV49	Q9tv49 cercocebus
17	606	32.7	339	6	Q9TUQ6	Q9tuq6 erythrocebu
18	606	32.7	352	6	Q95NE1	Q95ne1 cercocebus
19	605	32.6	352	6	O77776	O77776 cercocebus
20	604	32.6	339	6	Q9TQU7	Q9tqu7 cercopithec
21	604	32.6	339	6	Q9TSN2	Q9tsn2 macaca fasc
22	604	32.6	352	6	O97975	O97975 macaca arct
23	604	32.6	352	6	Q9TSK1	Q9tsk1 cercopithec
24	604	32.6	352	6	Q9TV42	Q9tv42 cercopithec
25	604	32.6	352	6	Q9XS99	Q9xs99 gorilla gor
26	604	32.6	352	6	Q95NE8	Q95ne8 cercopithec
27	604	32.6	352	6	Q95ND0	Q95nd0 erythrocebu
28	603	32.5	352	6	Q9XT12	Q9xt12 cercopithec
29	603	32.5	352	6	Q9BGN5	Q9bgn5 cercopithec
30	602	32.5	352	6	Q9TV50	Q9tv50 pan troglod
31	601	32.4	339	6	Q9TUW4	Q9tuw4 pan troglod
32	601	32.4	339	6	Q9TUS6	Q9tus6 papio cynoc
33	601	32.4	339	6	Q9TUS5	Q9tus5 papio cynoc
34	601	32.4	339	6	Q9TUR4	Q9tur4 mandrillus
35	601	32.4	352	6	Q95NC1	Q95nc1 theropithec
36	600	32.4	339	6	Q9TQX3	Q9tqx3 mandrillus
37	600	32.4	339	6	Q9TQX2	Q9tqx2 erythrocebu
38	600	32.4	339	6	Q9TQU5	Q9tqu5 cercopithec
39	600	32.4	339	6	Q9TQU4	Q9tqu4 cercopithec
40	600	32.4	339	6	Q9TQR2	Q9tqr2 gorilla gor
41	600	32.4	339	6	Q9TUW5	Q9tuw5 pan troglod
42	600	32.4	339	6	Q9TUT6	Q9tut6 macaca neme
43	600	32.4	352	6	Q9TQX0	Q9tqx0 cercopithec
44	600	32.4	352	6	Q95NC5	Q95nc5 hylobates s
45	600	32.4	352	6	Q95NC0	Q95nc0 hylobates m

ALIGNMENTS

RESULT 1
Q9UQQ6
ID Q9UQQ6 PRELIMINARY; PRT; 369 AA.
AC Q9UQQ6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE CHEMOKINE RECEPTOR CCR9 (CC CHEMOKINE RECEPTOR 9A).
GN CCR9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99248139; PubMed=10229797;
RA Zaballos A., Gutierrez J., Varona R., Ardavin C., Marquez G.;
RT "Identification of the orphan chemokine receptor GPR-9-6 as CCR9, the
RT receptor for the chemokine TECK.";
RL J. Immunol. 162:5671-5675(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Yu C.-R., Peden K.W.C., Farber J.M.;
RT "CCR9A and CCR9B, Two Receptors for the Chemokine CCL25 (TECK/Ckbeta-
RT 15).";
RL Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ132337; CAB43477.1; -.
DR EMBL; AF145439; AAF66699.1; -.
DR InterPro; IPR004069; Chemokine9_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 369 AA; 42015 MW; F27CEA0CFB66B44C CRC64;

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  Query Match           100.0%;  Score 1854;  DB 4;  Length 369;
  Best Local Similarity  100.0%;  Pred. No. 1e-164;
  Matches  357;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     13 MADDYGSESTSSMEDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILV 72

Qy     61 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 YWYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYS 132

Qy    121 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 CVLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEE 192

Qy    181 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 SGIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKA 252

Qy    241 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 LKVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCL 312

Qy    301 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 357
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 NPVLYVFVGERFRRDLVKTLKNLGCISQAQWVSFTRREGSLKLSSMLLETTSGALSL 369


RESULT   2
O42444
ID   O42444      PRELIMINARY;      PRT;   368 AA.
AC   O42444;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR.
OS   Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX   NCBI_TaxID=8022;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99260342; PubMed=10331499;
RA   Daniels G.D., Zou J., Charlemagne J., Partula S., Cunningham C.,
RA   Secombes C.J.;
RT   "Cloning of two chemokine receptor homologs (CXC-R4 and CC-R7) in
RT   rainbow trout Oncorhynchus mykiss.";
RL   J. Leukoc. Biol. 65:684-690(1999).
DR   EMBL; AJ003159; CAA05917.1; -.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   368 AA;  41523 MW;  BE28E2D4C47E821A CRC64;


  Query Match           41.9%;  Score 776.5;  DB 13;  Length 368;
  Best Local Similarity  43.6%;  Pred. No. 2.4e-64;
  Matches  157;  Conservative   73;  Mismatches  115;  Indels   15;  Gaps    6;

Qy      4 DYGSESTSSM-EDYVNFNFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILVY- 61
          || |  | :: || |:    :| |:|: || |   : ||||| : |:| |||  |: :|
Db     18 DYDSSFTPTVGEDDVD----NFMCDKSAVRAFRGQYEPPLYWSIVILGGLGNLTVVWIYL 73

Qy     62 WYCTRVKTMTDMFLLNLAIADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYSC 121
           :  |:|||||::|||||:||| || ||| ||: |   | |   :||| :: ||:||:|
Db     74 HFRQRLKTMTDIYLLNLAVADLFFLGTLPLWAVEANQGWSFGLGLCKVTSAFYKINFFSS 133

Qy    122 VLLIMCISVDRYIAIAQAMRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEES 181
          :||: |||||||: | |   |   : :||  || ||  :|:||  | :|| ::: :||
Db    134 MLLLTCISVDRYVVIVQTTMAQNSKRQRLSCSKFVCACVWLLAVLLALPEFMFANVKELD 193

Qy    182 GIAICTMVYPSDESTKLKSAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKAL 241
          |   ||||| |::: : |  || |:: :|| || :||  ||  || ||:: :   |||||
Db    194 GQFYCTMVYWSNQNNRTKIVVLGLQICMGFCLPLLVMVFCYAGIIRTLLKTRSFQKHKAL 253

Qy    242 KVTITVLTVFVLSQFPYNCILLVQTIDAYAMFISNCAVSTNIDICFQVTQTIAFFHSCLN 301
          :| : |: |||||| ||| :|:::   |     ::|: :   ::  || :::|: |:|||
Db    254 RVILVVVAVFVLSQLPYNSVLVMEATQAANSTQTDCSAAKRFNVVSQVLKSLAYTHACLN 313

Qy    302 PVLYVFVGERFRRDLVKTLKNLGCISQAQWVS---FTRREGSLKLSSMLLET-TSGALSL 357
          | |||||| |||||::| |:   |    | :     : :|    ||:: :| |: ||||
Db    314 PFLYVFVGVRFRRDILKLLRIYHC-----WPAKGKLRKIQGGPGRSSVMSDTDTTQALSL 368


RESULT   3
Q9EQ16
ID   Q9EQ16      PRELIMINARY;      PRT;   351 AA.
AC   Q9EQ16;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CHEMOKINE RECEPTOR CXCR6.
GN   CXCR6.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RX   MEDLINE=21177382; PubMed=11017100;
RA   Matloubian M., David A., Engel S., Ryan J.E., Cyster J.G.;
RT   "A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo.";
RL   Nat. Immunol. 1:298-304(2000).
DR   EMBL; AF301018; AAG34367.1; -.
DR   MGD; MGI:1934582; Cxcr6.
DR   InterPro; IPR000276; GPCR_Rhodpsn.
DR   Pfam; PF00001; 7tm_1; 1.
DR   PRINTS; PR00237; GPCRRHODOPSN.
DR   PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR   PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW   Receptor.
SQ   SEQUENCE   351 AA;  40468 MW;  5658788372B4C65A CRC64;


  Query Match           36.2%;  Score 671.5;  DB 11;  Length 351;
  Best Local Similarity  40.2%;  Pred. No. 1.4e-54;
  Matches  137;  Conservative   77;  Mismatches  102;  Indels   25;  Gaps    8;

Qy     20 NFTDFYCEKNNVRQFASHFLPPLYWLVFIVGALGNSLVILVYWYCTRVKTMTDMFLLNLA 79
          | :|   |     :|   ||| :| :||: | ||||||:::| :  :::|:||:|||||
Db     24 NSSDNSQENKRFLKFKEVFLPCVYLVVFVFGLLGNSLVLIIYIFYQKLRTLTDVFLLNLP 83

Qy     80 IADLLFLVTLPFWAIAAADQWKFQTFMCKVVNSMYKMNFYSCVLLIMCISVDRYIAIAQA 139
          :|||:|: ||||||  |   :| | | ||| :  || ||||  :| : ||:|||:| : ||
Db     84 LADLVFVCTLPFWAYAGTYEWVFGTVMCKTLRGMYTMNFYVSMLTLTCITVDRFIVVVQA 143

Qy    140 MRAHTWREKRLLYSKMVCFTIWVLAAALCIPEILYSQIKEESGIAICTMVYPSDESTKLK 199
          :|   : |  :: :::|  |||::  : :|:|:|  :::   :  ||   | ||:|   :
Db    144 TKAFNRQAKWKIWGQVICLLIWVVSLLVSLPQIIYGHVQDIDKL-ICQ--YHSEE---IS 197

Qy    200 SAVLTLKVILGFFLPFVVMACCYTIIIHTLIQAKKSSKHKALKVTITVLTVFVLSQFPYN 259
          : || ::: |||||| : |  ||: || ||: |:   |||:||:   |: ||:|:| |:|
Db    198 TMVLVIQMTLGFFLPLLTMILCYSGIIKTLLHARNFQKHKSLKIIFLVVAVFLLTQTPFN 257

Qy    260 CILLVQTI--DAYAMFISNCAVSTNIDICFQVTQTIAFFHSCLNPVLYVFVGERFRRDLV 317
            :|:|:   : | :         |:      ||: ||:| :|||||| ||| :||:::
Db    258 LAMLIQSTSWEYYTI--------TSFKYAIVVTEAIAYFRACLNPVLYAFVGLKFRKNVW 309

Qy    318 KTLKNLGCIS----QAQWVSFTRREGSLKL--SSMLLETTS 352
          | :|:::||:|     :|| |    | | |   :|  :||||
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